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GenCore version 5.1.3
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OM protein - nucleic search, using frame\_plus\_p2n model

January 16. 2003, 16.55.57; Search time 1056.51 Seconds (without alignments) 330.553 Million cell updates/sec Pun on:

1 EELMLRLQDYEE 12 US-09-856-070-21 60 Perfect score: Sednence:

BLOSUM62 Scoring table:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2054640 seqs, 14551402878 residues Searched:

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Command line parameters:

-MODEL frame.\_p2n.model - Div-x1p -Q-/rgn2\_1/USPTC\_spool/USEU86507c/runat\_1401.cus4\_16684d\_1541/app\_qucry.fasta\_1.1592 -Q--/rgn2\_1/USPTC\_spool/USEU86507c/runat\_1401.cus4\_16684d\_1541/app\_qucry.fasta\_1.1592 -D-CACEGERL GENETATA - EAGLE - STEEKX-4-Q--MINMACHAN-Human4n - Long-EAST-0--UNITS=blis -START+1 - END--1 - MATRIX=blosum62 - TPANS-human4n - di- TIST\_45 -DOCALIGN-200 - THR\_SCORE-pct - THR\_MAX=100 - THL\_MIN 0 - ALIGN-15 - MODE-LOAD - OUTPHT=pto. - NNEMEXIX - HAA/Sidb-7un - MIN EN=9 - MAXIAN=2 unanumun - USEP-ISGNGF607(\_min)N\_1 = 12574\_\_wrnnat\_14012\_uu\_1 = 165844\_\_b2\_1 - NIPU-3 - NO\_XIDPY - NO\_MMAP - LARGNOUEPY - NFG\_SCORES-0 - WAIT - LOAD:0.03 - OFY\_TIMEOUT=120 - WARN\_TIMEOUT=30 - THPEADS=1 - XVAROP=10 - XVAROP=10, S - PGAPOP=6 - PGAPEXI - 7

Database

em\_tun:\* em\_hum:\* em\_in:\* em\_pat:\* em\_ph:\* em\_pl:\* em\_ro:\* gb\_sy:\* gb\_un:\* gb\_vi:\* em\_sts:\* em\_un:\* gb\_pat.\* gb\_ph:\* gb\_p!:\* gb\_pr:\* qb\_sts:\* gb\_ba:\* gb\_htg:\* em\_om:\* gb\_in. \* em\_mu:\* #:ou=db em ba·∗ • ∴o-we GenEmbl:\*

em_vi:*	em_htg_hum:*	em_htg_inv:*	em_htg_other:*	em_htg_mus:*	em_htq_pln:*		em_htq_mam:*	em_htg_vrt:*	em_sy:*	em_htgo_hum:*	em_ht.go_mus:*	em_ht.go_ot.her:*
29:	30:	31:	32:	33:	34:	35:	36:	37:	38:	39:	40:	41:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		9			SUMMARIES	
Result No.	30016	Query Match	Length DB	DB	<u> </u>	bescription
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٦	57	95.0	286508		AC125143	
15	55	91.7			AF188897	Homo
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13	63	88.3	_		AC110744	_
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1.9	C)	7. 0.:			AF199015	
07	45	75.0			AB019790	Gallus
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7		73.3	_		AP003376	Oryza
52		73.3	186416	C1	AC011226	AC011226 Homo sapi
56		73.3	_		AC013786	Homo
27	1. ₹	70.0			AF004891	AF004891 Oryza sat.
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33		68.3			AC109211	Musn
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33			143794		AP004305	AP004305 Oryza sat.
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35			169047		AI.357935	AL357935 Human DNA
36		ж	173775		AC079933	AC079933 Trypanoso
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o'm			343		YSAALK2B	C.
40		٤	1089		HHU29448	3 80
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4		ي	1830	C1	AP004180	Oryga
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ALIGNMENTS

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Query Match:
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                                     FEATURES
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FGLQYVDNKGFPTWLKLDKKVSAQEVRKESPLQFKFRAKFYPEDVAEELIQDITGKLF
FLQVKEGILSDEIYGFPETAVLGSYAVQAKFGDYNKELHKAGYLGSFRLIPQRVMDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKLI KIJUWEDKI QVWHAEHKGMI,KOSAMI,EYLKI AQDLEMYGI NYFELKNKKGTDI,MI,
GVDALGI,NI YEKDDKLITPKI GEPWSEI RNI SENDKKEVIKPI DKKAPDEVVEYAPRI,RI
NKRI I GI.CMGNHEI YMRRRK PDTI EVQOMKAQAREEKHQKQI,ERQOLETEKKRRETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLAALRAKEELEKGAADQIKSQEQLATELAEYTÄKIALLEEARRKKENĒVEEMQIJRAK
EAQDDLVKTREELHLVMTAPPPPPVYEPVNYHVHEGPQEEGTELSAELSSEGILIJDRN
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ROGNTKOR LDEFRAM"
                 MAM 11-JUN-1993
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                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                      Hergson, C.M., Zhao, H., Saijoh, K., Duman, R.S. and Nestler, E.J., Erzin and ostconcerin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus Mol. Cell. Neurosci. 4, 64-73 (1993)
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 2930)
Turunca,o., Wingvist,R., PakkanomiR., Grzoschik,K.H., Wahlsfrom,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryola, Metazza; Chordata; Craniata; Vertebrata, Euteleosfomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cytovillin; cytovillin 2; microvillar protein.
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Mismatches:
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                               Bos taurus ezrin mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"czrin"
/protein_id-"AAA30510.1"
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               2514 bp
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1. .2514
/organism="Bos faurus"
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                                                                                                             Bos taurus brain cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="brain"
152. .1897
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                                                                                         KEYWORDS
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PTWILLDKKVSAGEVRRENITJÖF KERAFTPEDVARELLIGUTTOKLFFLIDVREGTLSD
ELYCPPETAVLLGSYAVQAREGDYNKEVHKSGYLSSERLI PORVMDOHKLTRDOMEDR
TOVWHAEFHROMLKDNAMLJYLKTAGDILEMYGTNYFFFTRNKKGTDILMIGVDALGILNTYF
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ELHLVMTAPPPPPPYYEPVSYHVOESLODEGAEPTGYSAELSSEG LRIDRNEFKR LT
FAEKNERVOROLYTLSSELSOARDENKRTHND LIHNENMROGEDKYKTLROTROGENTK
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ELMLRLQDYEEKTKKAERRLSFQTQRALQLEEERKRAQEEAERLEADRMAALRAKEEL
Draft entry and computer-readable sequence for [1] kindly submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDDKI TPKIGEPWSEIPNISENDKKFVIKPIPKKAPPFVFYAPRLPINKRILOLOMGN
                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MDAELEFAIQPNTTGKQLFDQVVKTIGLREVWYFGLHYVDNKGF
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref-"taxon:9606"
/note-"EMBL/GenBank Accession No. X51521"
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Patent: WO 0229103-A 3721 11-APR-2002;
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                                                                                        /organism≈"Homo sapiens"
/db_xref="taxon:9606"
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                      by O.Turunen, 31-AUG-1989.
Location/Qualitiers
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Fri Jan 17 09:18:52 2003

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Berlin-Charlottenburg, GERMANY, Email: clonewind.de Further
information about the clone and the sequencing project is available
at http://www.nips.biorten.npg.de/proj/ctna/.
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu.J., Witcham, Fl., Harlocker, S.F., Dillon, D.C., Secrist, H., Lodes, M.J., Algate, P.A., Filog, S.P., Mannion, J., Benson, D.R. and

    (bases 1 to 3072)
    Ottenwaelder, B., Obermaler, B., Mewes, H.W., Weil. B. and Wiemann, S.

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PDDRNEEKPTTEAEKNERVOPGLVTLSSELSGARDENKRTHNDIIHNENMRGGKOKYK
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Submitted (25.5M 1990) Hunter T., The Saik institute, Molecular
Biology and Virology Laboratory, 10010 North Terrey Pines Road, San
Diego, CA 92138, USA
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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Gould,K.L., Bretscher.A., Esch,F.S. and Hunter,T.
cDNA cloning and sequencing of the protein tyrosine kinase
substrate, ezrin, reveals homology to band 4.1
EMBO J. B (13), 4133-4142 (1989)
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Homo sapiens.
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/cell_line-"HeLa"
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WHAEHRGMLKDNAMLEYLKI AQDLEMYGINYFEI KNKRGTDLMLGVDALGLNI Y EKDD
KLIPKIGFPWSFI PNI SFNDKKFVI KPI DKYRAPPEVFYAPPLPINKPI LQICM"NHEL
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LRIOOVEEKTKKAEPET SEGTORALOTEEFPREAGEEARELADEMAALLAKEETLEKO
AVDOTKSGTOLAAELAEYTAKTALLEEARREKEDEVEEMQHRAKEAODIJVKTKEELH
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KNERVQRQLLTLSSELSJARDENKRTIIND I IHNENMPJGRDRYKTLEQIPJGINTRQPI
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Submitted (07-SEP-2001) National Institutes of Health, Mammalian
                                                                                  Alissue type-"melanoma (MeWo cell line)"
Actone_lib-"762 (synonym: hmel2). Vector pSportl; host
DHIOB; sites Not1 : Sal!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
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Homo Sapiens, Similar to villin 2 (exrin), clone McC:1584
IMARE:2999399, mKNA, Complete cds.
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Conservative:
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/organism-"Homo sapiens"
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                                         /map-"6q22-q27"
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                   /db xref="taxon.9606"
                                                                                                                                                                                                         /qene-"DKFZp762H157"
                                                                                                                                                                                                                                                       /gene-"DKFZp762H157"
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                                                                                                                                     DH10B; sites Noti +
/dev_stage="adult"
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polyA_site
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215705 bp DNA Titical PKL 15 SEP 2001
Human DNA sequence from clone RP11-507010 on chromosome 6q25.2-26,
ALSB9931 AC023785
HTG.
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FLGVKEGTLSDEIYCPPFTAVLLGSYAVQAKFGDYNKEVHKSGYLSSFRLIPQRVMDO
HKLTROQWEDKIQVWHAEHRGMIKDNAMLEYLKIAQDLEMYGINYFEIKNKKGTDLWL
                                                                                                                                               Clone distribution; MGC clone distribution information can be found
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REKEQMMREKEELMLRLODYEEKTKRAERELSEQTORALOLLEEERKRAQEEGAEKLEAD
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RIDPNFFKRTTEAEKNERVOROLLTLSSELSQARDENKFTHNDTTHNENMRQGPCKYK
TLRQTRQGNTKQRTDEFFAL."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MPKPINVRVTTMDAELEFAIGPNTTGK0LFDQVVKTIGLREVWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVDALGINTYEKDDKLIPKTGFPWSETRNTSFNDKKEVIKPTDKKAPDFVFYAPRIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMAALRAKEELERQAVDO 1 KSQEQLAAFLAFYTAK 1 ALLEEARREKEDEVEEWQHRAK
                                                                                                                                                                                                                        This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA qi: 9257254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requests: clonerequestissanger.ac.uk
On Sep 12, 2001 this sequence rersion replaced qi:14586238.
During sequence assembly data is compared from overlapping clones.
                                                                      Anup Madau, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      through the L.M.A.G.E. Consortium/Link at: http://image.llnl.gov
Series: IRAL Plate: 2 Row: a Column: 18
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DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org confact: amadamisystemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product-Similar to villin 2 (ezrin)"
/protein_id="AAH13903.1"
/db_xref="Gi:15530243"
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/clone="MGC:1584 IMAGE:2959499"
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Mismatches:
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/lab_host-"DH10B-R"
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Sehra,H.
Direct Submission
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together with a note of the corriging allowed many variation annotation and the corriginal allowed so we submit sequence submission corresponded to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate them stry or covered by hith quality data (i.e., pared quality >- 30); an attempt was made to resolve all sequencing problems, such as complement of the problems as the concept of the problems one plasmid subclone or more than one Mil subclone; and the assembly was continued by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMRI, Sw. Malabase, van he, formed in the vormed in the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sangerian.ok/Projects//Leingans/wormper.htms.sephonocass.ass.generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be Lound at.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear PRI 19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPI1-507C10 is from the library RPC: 11.2 constructed by the group of Pieter de Jong. For further details see http://www.ehori.org/barpac/home.htm

VECTOR: pBACe3.6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the entire insert of clone RPI1-507010 The true right end of clone RPI1-114MI1 is at 47323 in this sequence. Location/Qualifiers
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Restriction digest data confirm the assembly."
156422. 156454
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Where differences are found these are annotated as variations
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AF189213
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/db_xref="taxon-9606"
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/clone_lib="RPCI-11 2"
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A gene tamily consisting of ezrin, radixin and moesin. Its specific localization at actin filament/plasma membrane association sites 93055012
                                                                                                                                                                                                                                                                                                                         /protein_id="AAF03156.1"
/db_xrei="GI:6063147"
/translation=":SMYSINVFFTENFFGID:M:GV:ALGLM:YERROFLAFRIGEP
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IEVQQMRAQAREFKXQNQIPPQODIFIFKRRREXVEREKEQMMEKEBIMIRIQDYBD"
                                                                        Submitted (23-SEP-1999) OB/GYN, Yale University, 333 Cedar Street, New Haven, CT 06520, USA
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Eukaryota: Metacoa: Chordata: Craniata; Vertebrata; Euteleostomi:
Mammalia: Eutheria: Rodentia; Sciurognathi: Muridae: Musinae: Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Funayama,N., Nagafuchi,A., Sato,N., Tsukita,S. and Tsukita,S.
Radixin is a novel member of the band 4.1 family
J cell Eiol. 115 (4), 1039-1048 (1991)
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Submitted (12-701-1991) N. Funayama, National Inst. for
Physiological Sciences, Mycdairi Okaraki 444, JAPAN
2 (bases 1 to 2701)
                                                                                                                                                                                                                                                                                                                                                                                                                      2 others
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/note-"villin 2; kinase substrate"
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Mismatches:
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                   2 (backs 1 to 478)
Fadiei,A., Chen,Z.C. and Naftolin,F.
Direct Submission
                                                                                                                                                                                                                   /cell_line-"HL60"
/cell_type-"leukemia cells"
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Sato, N., Funayama. N.
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Unpublished
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Best Local Similari
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TITLE
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LÜDRAFFEKPTTPARKINERVÜĞÜLTILSINELSÇARPIFIKFTHINDI LHINENMPÇĞEPÜKYK
TERÇI KÇĞINEÇEK IDEFERAM*
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Mus musculus chromosome 16 clone RP23-3512, WORKING DRAFI SEQUENCE,
                                                                                                                                                                                                   /db_xref="SWLSS-PROT:P26049"
/translation="Mrhv:INVRVIIMDABLE:FALGEN:IGNOIFEGOVATIGEREVWY
                                                                                                                                                                                                                                                 FGLPYVDNKGFPTWLKLDKKVSAQEVRKENPVQFKFRAKFYPEDVAEELIGDIIGKLF
FLQVKDGILSDEIYCPPETAVLLGSYAVQAKFGDYNKFWHKSGYLSSEPLIPQHVWPVQ
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15.JAN-2001) Production Sequencing Facility, DCE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, JSA
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/protein_id="CAA43086.1"
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/db_xret-"taxon:10090"
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Center clone name: RPCI-23_35I2
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DOE Joint Genome Institute.
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Estimated insert size: 180802; sum-of-contias estimation quality coverage: 3.32 in Q20 bases; agarose-tp estimation Quality coverage: 3.34 in Q20 bases; sum of contias estimation. * NOTE: this is a * vote that the defect of the procest * consists of 26 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                         * arbitrary. Gaps between the contigs are represented as * runs ol N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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183362: contig of 41175 bp in length.
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contig of 1163 bp in length
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                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Enteleostomi, Mammalia; Eutheria: Rodentia: Sciurognathi; Muridae: Murinae: Mus. 1 (Dases I to 27782)

Han, J., Mentgerery, K. T., Grills, G., irov, F., Isray, J., Pomeranto, R., Gordon, M., Seller, J. Shim, C., heerkey, I., Thomas, F., Porora, A., and Kucherlapati, P., Porora, A., High, Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Han.J., Montgomery, R.T., Padigaru, M., Grills, G., Lee, E., Long, I., noshikhes, I.P. and Kucherlapati, P. Direct Submission.

Submisted (14-PEC-2001) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowno St., Cambridge, MA.
                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 207782)
Han J Montgomery K f , Grills, G , for, F , long, J , Pomerantz, P.
Han J Montgomery K f , Grills, G , for, F , I promas, E , Parria, A ,
Gordon, M , Goitz, J S and Kucheriapati, F
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-JUL-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Senome Center, Ison Morris Park Ave Bronx, NY 10461, USA (bases 1 to 207782)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary, gaps between the contras are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Oct 10, 1608 this sequence wershar replayed go 1074940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site http://www.hprsg.org/Shaparent/mouse.html
Contact:hpgemende.mgh.harvard.edu
------Shammary Statistics
Center project name: AED
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Chemistry: bye-terminator Big Dye; L00%
*Consensus quality: 18554 at least Q20
*Consensus quality: 177266 at least Q40
*Consensus quality: 64948 at least Q40
Estimated insert size: 206802 sum-of-contins
**Estimated insert size: 206802 sum-of-contins
 183302
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Quality coverage: 4.8x sum-of-contigs - N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Harvard Partners Genome Center Center
                         -000
                                                                                                                           Db 172991 GAGGAGTGATGTTCGCTCCACACTACAGCAC 173026
                         Conservative:
Mismatches:
                                                                                                              1 CluSlukeuMetkeuArgkeuGinAspTyrGluGke 12
              Matches.
 Length:
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                                                                                      US-09-856-070-21 (1-12) x ACOB7605 (1-183302)
                                                                                                                                                                                                                                                        HIG: HIGS_PHASE1; HT3S_DRAFT.
                                                                                                                                                                                                                                         AC074334.5 GI:10937966
1.8
57.00
joa no*
                                    91.678
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Best Local Similarity:
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Pred. No.:
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length

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Submitted (01:FEB:2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                  **Estimated instit size. agarose FF · N/A

**Estimated instit size. 217717 - sum-of-contigs
Quality coverage. agarose-FP - N/A
Quality coverage. 8.5 x in $20 bases, sum of contigs estimation
                                                            On Jan 4, 2002 this seganne version replaced gith094413,
                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence, it currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is abilitary. Says between the contigs are represented as fruns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                        Web site: http://www.hpcag.org/Sequence/mouse.html
Contact: hpge@mendel.mgh.harvard.edu
------Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60900: contiq of 60900 bp in length 60920: gap of unknown length 106520: contig of 45600 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 35782 bp in length
dap of unknown length
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contig of 28075 bp in length
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215820. gap of wiknown length
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Chemistry: Dye-terminator Big Dye: 100%
Consensus quality: 212564 at least 020
*Consensus quality: 21720 at least 040
*Consensus quality: 210797 at least 040
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142343. .176177
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/note∸"assembly_name:Contiq206"
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/note:"assembly_name:Contiq210
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/strain="C57BL6/J"
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/clone-"RP23-103120"
/sex "male"
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106541. .142322
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Mus musculus clone RP231[03120 strain C57816/71, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
1 (bases 1 to 21791?)
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                                     contiq of 1443 bp in length
gap of taknow length
                                                                                                                   195040: contiq of 1383 bp in length
195060: gap of unknown length
196945: contig of 1885 bp in length
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204170: qap of unknown length
205707: contig of 1537 bp in length
190625: contiq of 2715 bp in length
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gap of unknown length
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contig of 855 bp in length
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/chromosome-"15"
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Mus musculus chromosome UNF clone PP24-342H13, WopgIN: DPAFT AC12514.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus muscalus
Eukaryota: Metazea; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Pedestia, Sciuregnathi; Musidae, Musidae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 6.990319
Consensus quality: 289324 bases at least 040
Consensus quality: 285778 bases at least 040
Consensus quality: 286826 bases at least 020
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Sequencing vector: M13, 0%
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Contact: submissionsfwatson.wusfl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- Genome Center -----
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                               Gaps:
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HTG: HIGS_PHASF1; HTGS_DRAFT.
.234332
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\* NoTE: This is a 'working draft' sequence, It currently consists of 10 contigs. The true order of the pieces

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linear PRI 19-0CT-1999
* is not known and their order in this sequence record is arbitrary. Saps between the conligs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                          gap of unknown length
contig of 123560 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907 others
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gap of unknown length
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config of 1820; bp in length
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                                                                                                                                                                                                                                                                                                                                                      contig of 851 bp in length gap of unknown length contig of 1040 bp in length.
                                                                                                   1503: contig of 1503 bp in length
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contig of 2982 bp in length
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gap of unknown length
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of 26715 bp in
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40 c 136 g 93 t 2 others
                                                                                                                                                                                                                        Direct Submission
Submitted (22-SEP-1999) oB/GYN, Yale University, 333 Cedar Street,
New Haven, CT 06511, USA
                                               Homo sapiens.

Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 475)

Ezrin gene mutation in ovarian cancer
Unpublished

2 (bases 1 to 475)

Chen, 2.c., Fadiel, A. and Nattolin, F.

(chen, 2.c., Fadiel, A. and Nattolin, F.
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Mismatches:
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US-09-856-070 21 (1-12) x AF188897 (1-475)

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 Db
 443 GAGAGTTGATGCTGCGGCTGCAGGACTATGAA 475

Search completed: January 16, 2003, 19:04:48 Job time: 1120.51 sees